



2676-4555 seq listing v2.ST25
SEQUENCE LISTING

<110> Vlaams Interuniversitair Instituut Voor Biotechnologie VZW

<120> CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS

<130> 2676-4555US

<140> US 09/697,863

<141> 2000-10-27

<150> PCT/EP99/03025

<151> 1999-04-28

<150> EPO 98201392.2

<151> 1998-04-29

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1920

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1627)..(1627)

<223> N stands for any nucleotide.

<220>

<221> CDS

<222> (20)..(1108)

<223>

<220>

<221> misc_feature

<222> (1849)..(1849)

<223> N stands for any nucleotide.

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1 5 10

gag gcg gcg gag gaa gag ggc gag cct gag gtg aaa aag cgg cga ctt 100
Glu Ala Ala Glu Glu Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu
15 20 25

ctg tgt gtg gag ttt gcc tcg gtc gca agc tgc gat gcc gca gtg gct 148
Leu Cys Val Glu Phe Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala
30 35 40

cag tgc ttc ctg gcc gag aac gac tgg gag atg gaa agg gct ctg aac 196
Gln Cys Phe Leu Ala Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn
45 50 55

tcc tac ttc gag cct ccg gtg gag gag agc gcc ttg gaa cgc cga cct 244
Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro
60 65 70 75

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gaa acc atc tct gag ccc aag acc tat gtt gac cta acc aat gaa gaa 292
Glu Thr Ile Ser Glu Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu
80 85 90

aca act gat tcc acc act tct aaa atc agc cca tct gaa gat act cag 340
Thr Thr Asp Ser Thr Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln
95 100 105

caa gaa aat ggc agc atg ttc tct ctc att acc tgg aat att gat gga 388
Gln Glu Asn Gly Ser Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly
110 120

tta gat cta aac aat ctg tca gag agg gct cga ggg gtg tgt tcc tac 436
Leu Asp Leu Asn Asn Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr
125 130 135

tta gct ttg tac agc cca gat gtg ata ttt cta cag gaa gtt att ccc 484
Leu Ala Leu Tyr Ser Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro
140 145 150 155

cca tat tat agc tac cta aag aag aga tca agt aat tat gag att att 532
Pro Tyr Tyr Ser Tyr Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile
160 165 170

aca ggt cat gaa gaa gga tat ttc aca gct ata atg ttg aag aaa tca 580
Thr Gly His Glu Glu Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser
175 180 185

aga gtg aaa tta aaa agc caa gag att att cct ttt cca agt acc aaa 628
Arg Val Lys Leu Lys Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys
190 195 200

atg atg aga aac ctt tta tgt gtg cat gtg aat gtg tca gga aat gag 676
Met Met Arg Asn Leu Leu Cys Val His Val Asn Val Ser Gly Asn Glu
205 210 215

ctt tgc ctt atg aca tcc cat ttg gag agc acc aga ggg cat gct gcg 724
Leu Cys Leu Met Thr Ser His Leu Glu Ser Thr Arg Gly His Ala Ala
220 225 230 235

gaa cga atg aat cag tta aaa atg gtt tta aag aaa atg caa gag gct 772
Glu Arg Met Asn Gln Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala
240 245 250

cca gag tca gct aca gtt ata ttt gca gga gat aca aat cta agg gat 820
Pro Glu Ser Ala Thr Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp
255 260 265

cga gag gtt acc aga tgt ggt ggt tta ccc aac aac att gtg gat gtc 868
Arg Glu Val Thr Arg Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val
270 275 280

tgg gag ttt ttg ggc aaa cct aaa cat tgc cag tat aca tgg gat aca 916
Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr
285 290 295

caa atg aac tct aat ctt gga ata act gct gct tgt aaa ctt cgt ttt 964
Gln Met Asn Ser Asn Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe
300 305 310 315

gat cga ata ttt ttc aga gca gca gca gaa gag gga cac att att ccc 1012
Asp Arg Ile Phe Phe Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro
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BF
Cant

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320

325

330

cga agt ttg gac ctt ctt gga tta gaa aaa ctg gac tgt ggt aga ttt 1060
 Arg Ser Leu Asp Leu Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe
 335 340 345
 cct agt gat cac tgg ggt ctt ctg tgc aac tta gat ata ata ttg taa 1108
 Pro Ser Asp His Trp Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
 350 355 360
 aatgcttttc aagtgtgggt ttgcccctga ttgttgcaaa tacaatttcc accttctgga 1168
 aaggtagggt tgctgtggag gaaataatgt actagatcat tgtcacagaa aaaccaacta 1228
 tgatttatgg ttgtgttttc agaattcaac attaaagatt aatgtttatt taaacgaaca 1288
 cattcctgca ttcaggatgt gaggccattt aataaaaagg gcacaaagcc tgtcagagtt 1348
 ttcaacgggtg cttacagctg ccagctggat tccaaacagg tacccttggt tctctgagct 1408
 aatgtttata tttttccatt caggcaccga aatagttaat atttaaaata agtcttcaaa 1468
 agaaaacata agagattatt gagttcttgg gactggatcc tttatttcat aagttcagat 1528
 catcttaaat gaaaatgccg tgattatctg cagttaagta gatgacagct attctacatc 1588
 agacttgatt tttgtcagct aattacataa ttggtaagnt ataattgaaa ccttatggct 1648
 taaaattcct taactccttt ttgattcatg tttgtagtca tgttgtcaac agaggcaaa 1708
 ttaagcttga tgatgggtta aatcggtttg atagcaccat gggacatttt ttaacaaaa 1768
 ataatgcat gaagagacat agccttttag ttttgcta atgtgaaatgg aaatgcttta 1828
 caggaagtaa atgcaaatta nttttaagt tgctttaaag aaaaatattt tccccacagg 1888
 agaaatttaa ataaagaatt ttatttggtg aa 1920

<210> 2
 <211> 362
 <212> PRT
 <213> Homo sapiens

<400> 2

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1 5 10 15

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
20 25 30

Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
35 40 45

Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
50 55 60

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
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Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro Arg Ser Leu Asp Leu
325 330 335

Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe Pro Ser Asp His Trp
340 345 350

Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
355 360

<210> 3
<211> 1312
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (122)..(1234)
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aattcggcac gagggcgagg agcagcgtga agagcgggtg ttttgagggg accctgcggc 120
g atg gcg tct ggc agc agt tcc gat gcg gcg gag ccc gca ggg ccg gca 169
Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
1 5 10 15
ggg cgg gcg gcg tcg gcg ccc gaa gca gca cag gcg gag gag gac cgg 217
Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
20 25 30
gtg aag agg cgg cgg ctt cag tgc ctg ggc ttt gcg ttg gtg ggg gga 265
Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly
35 40 45
tgc gac ccc acg atg gtc ccc agc gtc ctg cgg gag aac gac tgg cag 313
Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp Gln
50 55 60
acg cag aaa gcc ctg agc gcc tac ttc gag ctg cca gag aac gac caa 361
Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln
65 70 75 80
ggg tgg ccg cgc cag cct ccc acg tcc ttc aag tcc gag gcc tat gtt 409
Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr Val
85 90 95
gat cta acc aac gag gat gca aat gat aca acc att tta gaa gcc agt 457
Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala Ser
100 105 110
cca tct gga act cct cta gaa gat agc agc act att tct ttc att acc 505
Pro Ser Gly Thr Pro Leu Glu Asp Ser Ser Thr Ile Ser Phe Ile Thr
115 120 125
tgg aat att gat gga tta gat gga tgc aat ctg ccc gag agg gct cga 553
Trp Asn Ile Asp Gly Leu Asp Gly Cys Asn Leu Pro Glu Arg Ala Arg
130 135 140

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ggg gtg tgt tcc tgc cta gct ttg tat agt cca gat gtg gta ttt cta 601
 Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu
 145 150 155 160
 cag gaa gtt atc ccc cca tac tgt gcc tac cta aag aag aga gca gcc 649
 Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala
 165 170 175
 agt tac aca att att aca ggt aat gaa gaa gga tat ttc aca gct ata 697
 Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile
 180 185 190
 cta ttg aag aaa gga aga gtg aaa ttt aaa agt cag gag att att cct 745
 Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro
 195 200 205
 ttt cca aat acc aaa atg atg aga aac ctg cta tgc gta aat gtg agt 793
 Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser
 210 215 220
 ttg ggt gga aat gaa ttt tgc ctt atg aca tcc cat ttg gag agc acc 841
 Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr
 225 230 235 240
 aga gaa cat tct gcg gaa cga ata aga caa tta aaa act gtt ctt gga 889
 Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly
 245 250 255
 aaa atg caa gag gct cca gat tca acc acg gtt ata ttt gca gga gat 937
 Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Ala Gly Asp
 260 265 270
 aca aat tta aga gat caa gaa gtt atc aaa tgt ggt ggt tta cct gac 985
 Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Gly Leu Pro Asp
 275 280 285
 aac gtt ttt gat gcc tgg gaa ttt tta ggc aaa cct aaa cat tgc cag 1033
 Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln
 290 295 300
 tat aca tgg gat acg aaa gca aat aac aac ctc agg atc cct gct gct 1081
 Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala
 305 310 315 320
 tat aag cat cgt ttt gat cga ata ttt ttc aga gca gaa gag ggg cac 1129
 Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His
 325 330 335
 ctt att cct caa agt tta gac ctt gtt ggg ttg gaa aaa ctg gac tgt 1177
 Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys
 340 345 350
 ggt aga ttt ccg agt gat cac tgg ggg ctc ttg tgc acc ttg aat gta 1225
 Gly Arg Phe Pro Ser Asp His Trp Gly Leu Leu Cys Thr Leu Asn Val
 355 360 365
 gta ttg tga aaagcttccc acttgcagct ttacacgttt gtagcacta 1274
 Val Leu
 370
 gtcttgaatt tgtgtaggtc tcaacctttc aggacatc 1312

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<210> 4
 <211> 370
 <212> PRT
 <213> Mus musculus

<400> 4

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Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly
 35 40 45

Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp Gln
 50 55 60

Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln
 65 70 75 80

Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr Val
 85 90 95

Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala Ser
 100 105 110

Pro Ser Gly Thr Pro Leu Glu Asp Ser Ser Thr Ile Ser Phe Ile Thr
 115 120 125

Trp Asn Ile Asp Gly Leu Asp Gly Cys Asn Leu Pro Glu Arg Ala Arg
 130 135 140

Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu
 145 150 155 160

Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala
 165 170 175

Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile
 180 185 190

Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro
 195 200 205

Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser
 210 215 220

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Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr
 225 230 235 240

Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly
 245 250 255

Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Ala Gly Asp
 260 265 270

Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Gly Leu Pro Asp
 275 280 285

Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln
 290 295 300

Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala
 305 310 315 320

Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His
 325 330 335

Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys
 340 345 350

Gly Arg Phe Pro Ser Asp His Trp Gly Leu Leu Cys Thr Leu Asn Val
 355 360 365

Val Leu
 370

<210> 5
 <211> 1536
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1530)..(1531)
 <223> N stands for any nucleotide.

<220>
 <221> CDS
 <222> (209)..(1534)
 <223>

<220>
 <221> misc_feature
 <222> (1392)..(1392)
 <223> N stands for any nucleotide.

<400> 5

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tttcgtctct ttccgccagt ggcctcccag ctcacgcagg ggcgggtccc ggtagcgcga	120
ggcgggtgcag ggcgggaagg ggagtgggtgg cggctgcggc agtagggaca gcaggagcag	180
tggtgctgtc agcgcggccg tcggagac atg gga gac ccg ggg tcg gaa ata	232
Met Gly Asp Pro Gly Ser Glu Ile	
1 5	
ata gaa tct gtc cct cca gct ggc cct gag gca tct gag tca aca acg	280
Ile Glu Ser Val Pro Pro Ala Gly Pro Glu Ala Ser Glu Ser Thr Thr	
10 15 20	
gat gaa aat gaa gac gac att cag ttt gtc agt gaa gga cca tcg aga	328
Asp Glu Asn Glu Asp Asp Ile Gln Phe Val Ser Glu Gly Pro Ser Arg	
25 30 35 40	
cct gtt ctt gaa tac atc gat ctg gtc tgt ggt gat gat gaa aac cct	376
Pro Val Leu Glu Tyr Ile Asp Leu Val Cys Gly Asp Asp Glu Asn Pro	
45 50 55	
agc gcc tat tat agt gat att ctg ttt cct aaa atg cca aaa cga cag	424
Ser Ala Tyr Tyr Ser Asp Ile Leu Phe Pro Lys Met Pro Lys Arg Gln	
60 65 70	
ggg gat ttt ttg cat ttt tta aat atg aag aag gtg aaa aca gac aca	472
Gly Asp Phe Leu His Phe Leu Asn Met Lys Lys Val Lys Thr Asp Thr	
75 80 85	
gaa aat aat gaa gtg agc aaa aat cac tgc aga ttg tct aag gca aag	520
Glu Asn Asn Glu Val Ser Lys Asn His Cys Arg Leu Ser Lys Ala Lys	
90 95 100	
gaa cca cat ttc gag tat ata gaa caa cca atc att gaa gaa aag cca	568
Glu Pro His Phe Glu Tyr Ile Glu Gln Pro Ile Ile Glu Glu Lys Pro	
105 110 115 120	
tca ctt tca tca aag aaa gaa ata gat aat ctt gtg ctt cca gat tgt	616
Ser Leu Ser Ser Lys Lys Glu Ile Asp Asn Leu Val Leu Pro Asp Cys	
125 130 135	
tgg aat gaa aaa caa gca ttt atg ttt aca gaa caa tac aaa tgg ctt	664
Trp Asn Glu Lys Gln Ala Phe Met Phe Thr Glu Gln Tyr Lys Trp Leu	
140 145 150	
gaa ata aaa gaa ggt aaa tta gga tgt aag gat tgt tca gca gtt cgg	712
Glu Ile Lys Glu Gly Lys Leu Gly Cys Lys Asp Cys Ser Ala Val Arg	
155 160 165	
cat ttg gga tcg aaa gca gaa aag cat gtc cat gtg tcc aag gaa tgg	760
His Leu Gly Ser Lys Ala Glu Lys His Val His Val Ser Lys Glu Trp	
170 175 180	
att gca tat tta gta acc cct aat ggc agt aat aaa act act agg caa	808
Ile Ala Tyr Leu Val Thr Pro Asn Gly Ser Asn Lys Thr Thr Arg Gln	
185 190 195 200	
gct tct cta cga aaa aaa att agg gaa cat gat gtt tct aaa gcc cat	856
Ala Ser Leu Arg Lys Lys Ile Arg Glu His Asp Val Ser Lys Ala His	
205 210 215	
ggg aaa att cag gat ttg tta aag gaa tca act aat gat tca att tgt	904

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Gly	Lys	Ile	Gln	Asp	Leu	Leu	Lys	Glu	Ser	Thr	Asn	Asp	Ser	Ile	Cys	
			220					225					230			
aat	tta	gtg	cat	aaa	caa	aat	aat	aaa	aat	att	gat	gct	act	gta	aaa	952
Asn	Leu	Val	His	Lys	Gln	Asn	Asn	Lys	Asn	Ile	Asp	Ala	Thr	Val	Lys	
		235					240					245				
gtt	ttc	aat	act	gtt	tac	agt	tta	gta	aaa	cat	aac	aga	cct	tta	tct	1000
Val	Phe	Asn	Thr	Val	Tyr	Ser	Leu	Val	Lys	His	Asn	Arg	Pro	Leu	Ser	
		250				255					260					
gat	att	gag	ggg	gca	aga	gaa	tta	cag	gaa	aaa	aat	gga	gag	gta	aat	1048
Asp	Ile	Glu	Gly	Ala	Arg	Glu	Leu	Gln	Glu	Lys	Asn	Gly	Glu	Val	Asn	
		265			270					275					280	
tgt	tta	aat	aca	cgt	tac	agt	gca	aca	aga	ata	gca	gaa	cat	att	gca	1096
Cys	Leu	Asn	Thr	Arg	Tyr	Ser	Ala	Thr	Arg	Ile	Ala	Glu	His	Ile	Ala	
				285					290					295		
aaa	gaa	atg	aag	atg	aag	ata	ttt	aag	aat	att	ata	gaa	gag	aat	gcc	1144
Lys	Glu	Met	Lys	Met	Lys	Ile	Phe	Lys	Asn	Ile	Ile	Glu	Glu	Asn	Ala	
			300					305					310			
aaa	atc	tgt	atc	ata	att	gat	gag	gca	tct	aca	gtt	tca	aag	aaa	acc	1192
Lys	Ile	Cys	Ile	Ile	Ile	Asp	Glu	Ala	Ser	Thr	Val	Ser	Lys	Lys	Thr	
		315					320					325				
acc	cta	gtg	att	tat	ctc	cag	tgc	aca	att	cag	tca	gct	cct	gca	cct	1240
Thr	Leu	Val	Ile	Tyr	Leu	Gln	Cys	Thr	Ile	Gln	Ser	Ala	Pro	Ala	Pro	
		330				335					340					
gtt	atg	tta	ttt	gtg	gct	tta	aaa	gaa	ttg	gtg	tca	act	ata	gca	gag	1288
Val	Met	Leu	Phe	Val	Ala	Leu	Lys	Glu	Leu	Val	Ser	Thr	Ile	Ala	Glu	
		345			350					355					360	
tgt	att	gtc	aat	aca	tta	ttg	act	act	tta	aat	gat	tgt	ggt	ttt	aca	1336
Cys	Ile	Val	Asn	Thr	Leu	Leu	Thr	Thr	Leu	Asn	Asp	Cys	Gly	Phe	Thr	
				365					370					375		
aat	gaa	tat	ttg	aaa	gca	aat	tta	att	gca	ttt	tgt	tct	gat	ggt	gct	1384
Asn	Glu	Tyr	Leu	Lys	Ala	Asn	Leu	Ile	Ala	Phe	Cys	Ser	Asp	Gly	Ala	
			380					385					390			
aat	aca	anc	ctg	gga	aga	aag	tct	gga	gta	gct	aca	aaa	ttg	tta	gaa	1432
Asn	Thr	Xaa	Leu	Gly	Arg	Lys	Ser	Gly	Val	Ala	Thr	Lys	Leu	Leu	Glu	
		395					400					405				
aat	ttt	cct	gaa	atc	atc	att	tgg	aac	tgt	tta	aat	cat	cga	tta	caa	1480
Asn	Phe	Pro	Glu	Ile	Ile	Ile	Trp	Asn	Cys	Leu	Asn	His	Arg	Leu	Gln	
		410				415					420					
ttg	tca	ctt	gat	gat	tct	ata	tcc	gaa	ata	aaa	caa	att	aat	cat	tta	1528
Leu	Ser	Leu	Asp	Asp	Ser	Ile	Ser	Glu	Ile	Lys	Gln	Ile	Asn	His	Leu	
		425			430					435					440	
ann	tat	aa														1536
Xaa	Tyr															

<210> 6
 <211> 442
 <212> PRT

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<213> Homo sapiens

<220>

<221> misc_feature

<222> (395)..(395)

<223> The 'Xaa' at location 395 stands for Asn, Ser, Thr, or Ile.

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<222> (441)..(441)

<223> The 'Xaa' at location 441 stands for Lys, Asn, Arg, Ser, Thr, Ile, or Met.

<400> 6

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20 25 30

Phe Val Ser Glu Gly Pro Ser Arg Pro Val Leu Glu Tyr Ile Asp Leu
35 40 45

Val Cys Gly Asp Asp Glu Asn Pro Ser Ala Tyr Tyr Ser Asp Ile Leu
50 55 60

Phe Pro Lys Met Pro Lys Arg Gln Gly Asp Phe Leu His Phe Leu Asn
65 70 75 80

Met Lys Lys Val Lys Thr Asp Thr Glu Asn Asn Glu Val Ser Lys Asn
85 90 95

His Cys Arg Leu Ser Lys Ala Lys Glu Pro His Phe Glu Tyr Ile Glu
100 105 110

Gln Pro Ile Ile Glu Glu Lys Pro Ser Leu Ser Ser Lys Lys Glu Ile
115 120 125

Asp Asn Leu Val Leu Pro Asp Cys Trp Asn Glu Lys Gln Ala Phe Met
130 135 140

Phe Thr Glu Gln Tyr Lys Trp Leu Glu Ile Lys Glu Gly Lys Leu Gly
145 150 155 160

Cys Lys Asp Cys Ser Ala Val Arg His Leu Gly Ser Lys Ala Glu Lys
165 170 175

His Val His Val Ser Lys Glu Trp Ile Ala Tyr Leu Val Thr Pro Asn
180 185 190

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Gly Ser Asn Lys Thr Thr Arg Gln Ala Ser Leu Arg Lys Lys Ile Arg
195 200 205

Glu His Asp Val Ser Lys Ala His Gly Lys Ile Gln Asp Leu Leu Lys
210 215 220

Glu Ser Thr Asn Asp Ser Ile Cys Asn Leu Val His Lys Gln Asn Asn
225 230 235 240

Lys Asn Ile Asp Ala Thr Val Lys Val Phe Asn Thr Val Tyr Ser Leu
245 250 255

Val Lys His Asn Arg Pro Leu Ser Asp Ile Glu Gly Ala Arg Glu Leu
260 265 270

Gln Glu Lys Asn Gly Glu Val Asn Cys Leu Asn Thr Arg Tyr Ser Ala
275 280 285

Thr Arg Ile Ala Glu His Ile Ala Lys Glu Met Lys Met Lys Ile Phe
290 295 300

Lys Asn Ile Ile Glu Glu Asn Ala Lys Ile Cys Ile Ile Ile Asp Glu
305 310 315 320

Ala Ser Thr Val Ser Lys Lys Thr Thr Leu Val Ile Tyr Leu Gln Cys
325 330 335

Thr Ile Gln Ser Ala Pro Ala Pro Val Met Leu Phe Val Ala Leu Lys
340 345 350

Glu Leu Val Ser Thr Ile Ala Glu Cys Ile Val Asn Thr Leu Leu Thr
355 360 365

Thr Leu Asn Asp Cys Gly Phe Thr Asn Glu Tyr Leu Lys Ala Asn Leu
370 375 380

Ile Ala Phe Cys Ser Asp Gly Ala Asn Thr Xaa Leu Gly Arg Lys Ser
385 390 395 400

Gly Val Ala Thr Lys Leu Leu Glu Asn Phe Pro Glu Ile Ile Ile Trp
405 410 415

Asn Cys Leu Asn His Arg Leu Gln Leu Ser Leu Asp Asp Ser Ile Ser
420 425 430

Glu Ile Lys Gln Ile Asn His Leu Xaa Tyr
435 440

2676-4555 seq listing v2.ST25

B1
Conclude